

SEQUENCE LISTING

<110> Kato, Seishi
Sekine, Shingo

<120> HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND
CDNAS ENCODING THESE PROTEINS

<130> GIN-6710CPUS

<140> 09/529,100
<141> 2000-08-21

<150> JP 0276269
<151> 1997-10-08

<150> PCT/JP98/04474
<151> 1998-10-05

<160> 28

<170> PatentIn Ver. 2.0

<210> 1
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<212> PRT
<213> Homo sapiens

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Pro Gly Asp Leu Ile Glu Val Phe Arg Pro Gly Tyr Gln His Trp Ala
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Leu Tyr Leu Gly Asp Gly Tyr Val Ile Asn Ile Ala Pro Val Asp Gly
35 40 45
Ile Pro Ala Ser Phe Thr Ser Ala Lys Ser Val Phe Ser Ser Lys Ala
50 55 60
Leu Val Lys Met Gln Leu Leu Lys Asp Val Val Gly Asn Asp Thr Tyr
65 70 75 80
Arg Ile Asn Asn Lys Tyr Asp Glu Thr Tyr Pro Pro Leu Pro Val Glu
85 90 95
Glu Ile Ile Lys Arg Ser Glu Phe Val Ile Gly Gln Glu Val Ala Tyr
100 105 110
Asn Leu Leu Val Asn Asn Cys Glu His Phe Val Thr Leu Leu Arg Tyr
115 120 125
Gly Glu Gly Val Ser Glu Gln Ala Asn Arg Ala Ile Ser Thr Val Glu
130 135 140
Phe Val Thr Ala Ala Val Gly Val Phe Ser Phe Leu Gly Leu Phe Pro

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Lys Gly Gln Arg Ala Lys Tyr Tyr
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<213> Homo sapiens

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Val Ile His Leu Ala Pro Pro Ser Glu Tyr Pro Gly Ala Gly Ser Ser
35 40 45

Ser Val Phe Ser Val Leu Ser Asn Ser Ala Glu Val Lys Arg Glu Arg
50 55 60

Leu Glu Asp Val Val Gly Gly Cys Cys Tyr Arg Val Asn Asn Ser Leu
65 70 75 80

Asp His Glu Tyr Gln Pro Arg Pro Val Glu Val Ile Ile Ser Ser Ala
85 90 95

Lys Glu Met Val Gly Gln Lys Met Lys Tyr Ser Ile Val Ser Arg Asn
100 105 110

Cys Glu His Phe Val Thr Gln Leu Arg Tyr Gly Lys Ser Arg Cys Lys
115 120 125

Gln Val Glu Lys Ala Lys Val Glu Val Gly Val Ala Thr Ala Leu Gly
130 135 140

Ile Leu Val Val Ala Gly Cys Ser Phe Ala Ile Arg Arg Tyr Gln Lys
145 150 155 160

Lys Ala Thr Ala

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<213> Homo sapiens

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20 25 30

Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr
35 40 45

Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala
50 55 60

Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val
65 70 75 80

Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu Gly Gly Cys Ala
85 90 95

Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr Gly Ile Gly Ala
100 105 110

Ala Ala Cys Val Tyr Phe Gly Ile Ala Ala Ser Leu Val Lys Met Gly
115 120 125

Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys Val
130 135 140

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<213> Homo sapiens

<400> 4

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20 25 30

Glu Glu Asp Asp Asp Glu Glu Leu Asp Glu Thr Leu Ser Glu Arg Leu
35 40 45

Trp Gly Leu Thr Glu Met Phe Pro Glu Arg Val Arg Ser Ala Ala Gly
50 55 60

Ala Thr Phe Asp Leu Ser Leu Phe Val Ala Gln Lys Met Tyr Arg Phe
65 70 75 80

Ser Arg Ala Ala Leu Trp Ile Gly Thr Thr Ser Phe Met Ile Leu Val
85 90 95

Leu Pro Val Val Phe Glu Thr Glu Lys Leu Gln Met Glu Gln Gln
100 105 110

Gln Leu Gln Gln Arg Gln Ile Leu Leu Gly Pro Asn Thr Gly Leu Ser
115 120 125

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130 135 140

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<213> Homo sapiens

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20 25 30

Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp Gly Cys Ser Pro Asn Lys
35 40 45

Met Lys Thr Val Lys Cys Ala Pro Gly Val Asp Val Cys Thr Glu Ala
50 55 60

Val Gly Ala Val Glu Thr Ile His Gly Gln Phe Ser Leu Ala Val Arg
65 70 75 80

Gly Cys Gly Ser Gly Leu Pro Gly Lys Asn Asp Arg Gly Leu Asp Leu
85 90 95

His Gly Leu Leu Ala Phe Ile Gln Leu Gln Gln Cys Ala Gln Asp Arg
100 105 110

Cys Asn Ala Lys Leu Asn Leu Thr Ser Arg Ala Leu Asp Pro Ala Gly
115 120 125

Asn Glu Ser Ala Tyr Pro Pro Asn Gly Val Glu Cys Tyr Ser Cys Val
130 135 140

Gly Leu Ser Arg Glu Ala Cys Gln Gly Thr Ser Pro Pro Val Val Ser
145 150 155 160

Cys Tyr Asn Ala Ser Asp His Val Tyr Lys Gly Cys Phe Asp Gly Asn
165 170 175

Val Thr Leu Thr Ala Ala Asn Val Thr Val Ser Leu Pro Val Arg Gly
180 185 190

Cys Val Gln Asp Glu Phe Cys Thr Arg Asp Gly Val Thr Gly Pro Gly
195 200 205

Phe Thr Leu Ser Gly Ser Cys Cys Gln Gly Ser Arg Cys Asn Ser Asp
210 215 220

Leu Arg Asn Lys Thr Tyr Phe Ser Pro Arg Ile Pro Pro Leu Val Arg
225 230 235 240

Leu Pro Pro Pro Glu Pro Thr Thr Val Ala Ser Thr Thr Ser Val Thr
245 250 255

Thr Ser Thr Ser Ala Pro Val Arg Pro Thr Ser Thr Thr Lys Pro Met
260 265 270

Pro Ala Pro Thr Ser Gln Thr Pro Arg Gln Gly Val Glu His Glu Ala
275 280 285

Ser Arg Asp Glu Glu Pro Arg Leu Thr Gly Gly Ala Ala Gly His Gln
290 295 300

Asp Arg Ser Asn Ser Gly Gln Tyr Pro Ala Lys Gly Gly Pro Gln Gln
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Pro His Asn Lys Gly Cys Val Ala Pro Thr Ala Gly Leu Ala Ala Leu
325 330 335

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340 345

<210> 6

<211> 66

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<213> Homo sapiens

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Asn Ile Thr Gln Arg Gly Asn Val Ala Lys Thr Ser Arg Asn Ala Pro
20 25 30

Glu Glu Lys Ala Ser Val Gly Pro Trp Leu Leu Ala Leu Phe Ile Phe
35 40 45

Val Val Cys Gly Ser Ala Ile Phe Gln Ile Ile Gln Ser Ile Arg Met
50 55 60

Gly Met

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<212> DNA

<213> Homo sapiens

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atcaacatag cacctgtaga tggcattcct gcgtccttta caagcgccaa gtctgtattc 180

agcagtaagg ccctggtgaa aatgcagctc ttgaaggatg ttgtggaaa tgacacatac 240

agaataaaaca ataaatacga tgaaacgtac cccctctcc ctgtggaaaga aatcataaag 300

cggtcagagt ttgtaattgg acaggaggtg gcctataact tacttgtcaa caactgtgaa 360

cattttgtga cattgcttcg ctatggagaa ggagttcag agcaggccaa ccgagcgata 420

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aaaggacaaa gagcaaaata ctat 504

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<211> 492
<212> DNA
<213> Homo sapiens

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gagtaccccg gggctggctc ctccagtgtc ttctcagtcc tgagcaacag tgcagaggtg 180
aaacgggagc gcctggaaga tgtggtggga ggctgttgct atcgggtcaa caacagctg 240
gaccatgagt accaaccacg gcccgtggag gtgatcatca gttctgcgaa ggagatggtt 300
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agatatggca agtcccgctg taaacaggtg gaaaaggcca aggttgaagt cggtgtggcc 420
acggcgcttg gaatcctggt tgttgctgga tgctctttg cgattaggag atacaaaaaa 480
aaagcgacag cc 492

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<212> DNA
<213> Homo sapiens

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gtcacactca atcctccggg caccttcctt gaaggagtgg ctaaggttg acaatacacg 180
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cgcgagaagc ccgacgaccc cctgaactac ttcctcggtg gctgcgcgg aggctgact 300
ctgggagcac gcacgcacaa ctacgggatt ggcgcgcggc cctgcgtgtta cttggcata 360
gcggcctccc tggtaagat gggccggctg gagggctggg aggtgtttgc aaaacccaag 420
gtg 423

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<212> DNA

<213> Homo sapiens

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gatgagaccc tgtcgagag actatggggc ctgacggaga tgttccgga gagggtccgg 180
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tttgagacgg agaagttgca aatggagcaa cagcagcaac tgcagcagcg gcagatactt 360
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aagatc . . . 426

<210> 11

<211> 1038

<212> DNA

<213> Homo sapiens

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gatgacggat gctccccgaa caagatgaag acagtgaagt gcgcgcccgg cgtggacgtc 180
tgcaccgagg ccgtgggggc ggtggagacc atccacggac aattctcgct ggcagtgcgg 240
ggttgcgggtt cgggactccc cggcaagaat gaccgcggcc tggatcttca cgggcttctg 300
gcgttcatcc agctgcagca atgcgctcag gatcgctgca acgccaagct caacctcacc 360
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tacagctgtg tgggcctgag ccgggaggcg tgccaggta catgcggcc ggtcgtgagc 480
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gcagctaattg tgactgtgtc cttgcctgtc cggggctgtg tccaggatga attctgcact 600
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gctggccacc aggaccgcag caattcaggg cagtatcctg caaaaggggg gccccagcag 960

ccccataata aaggctgtgt ggctcccaca gctggattgg cagccttct gttggccgtg 1020
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<213> Homo sapiens

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cgccggcaacg tcgccaagac ctcgagaaat gcccccaag agaaggcgtc tgttaggaccc 120
tggttattgg ctctcttcat ttttgggtgc tgtggttctg caattttcca gattattcaa 180
agtatcagga tggcatg 198

<210> 13
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (212)..(715)

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ggcaaggctcg gcagactgcga ggccaagaga gacccagga cacacacagc tgccctcccg 180
tgcgagaaga agaccccgcc ttgagagtga g atg gcg ttt aat gat tgc ttc 232
Met Ala Phe Asn Asp Cys Phe
1 5

agt ttg aac tac cct ggc aac ccc tgc cca ggg gac ttg atc gaa gtg 280
Ser Leu Asn Tyr Pro Gly Asn Pro Cys Pro Gly Asp Leu Ile Glu Val
10 15 20

ttc cgt cct ggc tat cag cac tgg gcc ctg tac ttg ggt gat ggt tac 328
Phe Arg Pro Gly Tyr Gln His Trp Ala Leu Tyr Leu Gly Asp Gly Tyr
25 30 35

gtt atc aac ata gca cct gta gat ggc att cct gcg tcc ttt aca agc 376
Val Ile Asn Ile Ala Pro Val Asp Gly Ile Pro Ala Ser Phe Thr Ser
40 45 50 55

gcc aag tct gta ttc agc agt aag gcc ctg gtg aaa atg cag ctc ttg 424
Ala Lys Ser Val Phe Ser Ser Lys Ala Leu Val Lys Met Gln Leu Leu
60 65 70

aag gat gtt gtg gga aat gac aca tac aga ata aac aat aaa tac gat 472
Lys Asp Val Val Gly Asn Asp Thr Tyr Arg Ile Asn Asn Lys Tyr Asp
75 80 85

gaa acg tac ccc cct ctc cct gtg gaa gaa atc ata aag cgg tca gag 520
Glu Thr Tyr Pro Pro Leu Pro Val Glu Glu Ile Ile Lys Arg Ser Glu
90 95 100

ttt gta att gga cag gag gtg gcc tat aac tta ctt gtc aac aac tgt 568
Phe Val Ile Gly Gln Glu Val Ala Tyr Asn Leu Leu Val Asn Asn Cys
105 110 115

gaa cat ttt gtg aca ttg ctt cgc tat gga gaa gga gtt tca gag cag 616
Glu His Phe Val Thr Leu Leu Arg Tyr Gly Glu Gly Val Ser Glu Gln
120 125 130 135

gcc aac cga gcg ata agt acc gtt gag ttt gtg aca gct gct gtt ggt 664
Ala Asn Arg Ala Ile Ser Thr Val Glu Phe Val Thr Ala Ala Val Gly
140 145 150

gtc ttc tca ttc ctg ggc ttg ttt cca aaa gga caa aga gca aaa tac 712
Val Phe Ser Phe Leu Gly Leu Phe Pro Lys Gly Gln Arg Ala Lys Tyr
155 160 165

tat taacaattta ccaaagagat attgatattg aaggaatttg ggaggaggaa 765
Tyr

aagaaaacctg gggtaatac ttatttcag tgcatttcata ctgttccaga ttccatgtat 825
ggatggcaga ctcttaata aattgcttac tgatattatc tt 867

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<211> 168
<212> PRT
<213> Homo sapiens

<400> 14
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20 25 30

Leu Tyr Leu Gly Asp Gly Tyr Val Ile Asn Ile Ala Pro Val Asp Gly
35 40 45

Ile Pro Ala Ser Phe Thr Ser Ala Lys Ser Val Phe Ser Ser Lys Ala
50 55 60

Leu Val Lys Met Gln Leu Leu Lys Asp Val Val Gly Asn Asp Thr Tyr
65 70 75 80

Arg Ile Asn Asn Lys Tyr Asp Glu Thr Tyr Pro Pro Leu Pro Val Glu
85 90 95

Glu Ile Ile Lys Arg Ser Glu Phe Val Ile Gly Gln Glu Val Ala Tyr

100 105 110
Asn Leu Leu Val Asn Asn Cys Glu His Phe Val Thr Leu Leu Arg Tyr
115 120 125
Gly Glu Gly Val Ser Glu Gln Ala Asn Arg Ala Ile Ser Thr Val Glu
130 135 140
Phe Val Thr Ala Ala Val Gly Val Phe Ser Phe Leu Gly Leu Phe Pro
145 150 155 160
Lys Gly Gln Arg Ala Lys Tyr Tyr
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<211> 720
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<220>
<221> CDS
<222> (25)..(516)

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cct gga gac ctg att gag att ttc cgc ctt ggc tat gag cac tgg gcc 99
Pro Gly Asp Leu Ile Glu Ile Phe Arg Leu Gly Tyr Glu His Trp Ala
10 15 20 25
ctg tat ata gga gat ggc tac gtg atc cat ctg gct cct cca agt gag 147
Leu Tyr Ile Gly Asp Gly Tyr Val Ile His Leu Ala Pro Pro Ser Glu
30 35 40
tac ccc ggg gct ggc tcc tcc agt gtc ttc tca gtc ctg agc aac agt 195
Tyr Pro Gly Ala Gly Ser Ser Val Phe Ser Val Leu Ser Asn Ser
45 50 55
gca gag gtg aaa cgg gag cgc ctg gaa gat gtg gtg gga ggc tgt tgc 243
Ala Glu Val Lys Arg Glu Arg Leu Glu Asp Val Val Gly Gly Cys Cys
60 65 70
tat cgg gtc aac aac agc ttg gac cat gag tac caa cca cgg ccc gtg 291
Tyr Arg Val Asn Asn Ser Leu Asp His Glu Tyr Gln Pro Arg Pro Val
75 80 85
gag gtg atc atc agt tct gcg aag gag atg gtt ggt cag aag atg aag 339
Glu Val Ile Ile Ser Ser Ala Lys Glu Met Val Gly Gln Lys Met Lys
90 95 100 105
tac agt att gtg agc agg aac tgt gag cac ttt gtc acc cag ctg aga 387
Tyr Ser Ile Val Ser Arg Asn Cys Glu His Phe Val Thr Gln Leu Arg
110 115 120

tat ggc aag tcc cgc tgt aaa cag gtg gaa aag gcc aag gtt gaa gtc 435
 Tyr Gly Lys Ser Arg Cys Lys Gln Val Glu Lys Ala Lys Val Glu Val
 125 130 135

ggt gtg gcc acg gcg ctt gga atc ctg gtt gtc gct gga tgc tct ttt 483
 Gly Val Ala Thr Ala Leu Gly Ile Leu Val Val Ala Gly Cys Ser Phe
 140 145 150

gcg att agg aga tac caa aaa aaa gcg aca gcc tgaagcagcc acaaaatcct 536
 Ala Ile Arg Arg Tyr Gln Lys Lys Ala Thr Ala
 155 160

gtgttagaag cagctgtggg ggtcccagtg gagatgagcc tccccatgc ctccagcagc 596
 ctgaccctcg tgccctgtct caggcggtct ctagatcctt tcctctgttt ccctctctcg 656
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<210> 16
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 <212> PRT
 <213> Homo sapiens

<400> 16
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 20 25 30

Val Ile His Leu Ala Pro Pro Ser Glu Tyr Pro Gly Ala Gly Ser Ser
 35 40 45

Ser Val Phe Ser Val Leu Ser Asn Ser Ala Glu Val Lys Arg Glu Arg
 50 55 60

Leu Glu Asp Val Val Gly Gly Cys Cys Tyr Arg Val Asn Asn Ser Leu
 65 70 75 80

Asp His Glu Tyr Gln Pro Arg Pro Val Glu Val Ile Ile Ser Ser Ala
 85 90 95

Lys Glu Met Val Gly Gln Lys Met Lys Tyr Ser Ile Val Ser Arg Asn
 100 105 110

Cys Glu His Phe Val Thr Gln Leu Arg Tyr Gly Lys Ser Arg Cys Lys
 115 120 125

Gln Val Glu Lys Ala Lys Val Glu Val Gly Val Ala Thr Ala Leu Gly
 130 135 140

Ile Leu Val Val Ala Gly Cys Ser Phe Ala Ile Arg Arg Tyr Gln Lys
 145 150 155 160

Lys Ala Thr Ala

<210> 17
<211> 566
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (74)..(496)

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gagattgcgg gct atg gcg ccg aag gtt ttt cgt cag tac tgg gat atc 109
Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile
1 5 10
ccc gat ggc acc gat tgc cac cgc aaa gcc tac agc acc acc agt att 157
Pro Asp Gly Thr Asp Cys His Arg Lys Ala Tyr Ser Thr Ser Ile
15 20 25
gcc agc gtc gct ggc ctg acc gcc gct gcc tac aga gtc aca ctc aat 205
Ala Ser Val Ala Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn
30 35 40
cct ccg ggc acc ttc ctt gaa gga gtg gct aag gtt gga caa tac acg 253
Pro Pro Gly Thr Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr
45 50 55 60
ttc act gca gct gtc ggg gcc gtg ttt ggc ctc acc acc tgc atc 301
Phe Thr Ala Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile
65 70 75
agc gcc cat gtc cgc gag aag ccc gac gac ccc ctg aac tac ttc ctc 349
Ser Ala His Val Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu
80 85 90
ggc tgc gcc gga ggc ctg act ctg gga gca cgc acg cac aac tac 397
Gly Gly Cys Ala Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr
95 100 105
ggg att ggc gcc gcc tgc gtg tac ttt ggc ata gcg gcc tcc ctg 445
Gly Ile Gly Ala Ala Ala Cys Val Tyr Phe Gly Ile Ala Ala Ser Leu
110 115 120
gtc aag atg ggc cgg ctg gag ggc tgg gag gtg ttt gca aaa ccc aag 493
Val Lys Met Gly Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys
125 130 135 140
gtg tgagccctgt gcctgccggg acctccagcc tgcagaatgc gtccagaaat 546
Val
aaattctgtg tctgtgtgtg 566

<210> 18
<211> 141
<212> PRT
<213> Homo sapiens

<400> 18
Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr
1 5 10 15
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20 25 30
Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr
35 40 45
Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala
50 55 60
Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val
65 70 75 80
Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu Gly Gly Cys Ala
85 90 95
Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr Gly Ile Gly Ala
100 105 110
Ala Ala Cys Val Tyr Phe Gly Ile Ala Ala Ser Leu Val Lys Met Gly
115 120 125
Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys Val
130 135 140

<210> 19
<211> 1078
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (5)..(430)

<400> 19
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Met Ala Ala Ala Val Ala Ala Ala Gly Ala Gly Glu Pro Gln Ser
1 5 10 15
ccg gac gaa ttg ctc ccg aaa ggc gac gcg gag aag cct gag gag gag 97
Pro Asp Glu Leu Leu Pro Lys Gly Asp Ala Glu Lys Pro Glu Glu Glu
20 25 30
ctg gag gag gac gac gat gag gag cta gat gag acc ctg tcg gag aga 145
Leu Glu Glu Asp Asp Asp Glu Glu Leu Asp Glu Thr Leu Ser Glu Arg
35 40 45

cta tgg ggc ctg acg gag atg ttt ccg gag agg gtc cg^g tcc gc^g gcc 193
Leu Trp Gly Leu Thr Glu Met Phe Pro Glu Arg Val Arg Ser Ala Ala
50 55 60

gga gcc act ttt gat ctt tcc ctc ttt gtg gct cag aaa atg tac agg 241
Gly Ala Thr Phe Asp Leu Ser Leu Phe Val Ala Gln Lys Met Tyr Arg
65 70 75

ttt tcc agg gca gcc ttg tgg att ggg acc act tcc ttt atg atc ctg 289
Phe Ser Arg Ala Ala Leu Trp Ile Gly Thr Thr Ser Phe Met Ile Leu
80 85 90 95

gtt ctt ccc gtt gtc ttt gag acg gag aag ttg caa atg gag caa cag 337
Val Leu Pro Val Val Phe Glu Thr Glu Lys Leu Gln Met Glu Gln Gln
100 105 110

cag caa ctg cag cag cg^g cag ata ctt cta gga cct aac aca ggg ctc 385
Gln Gln Leu Gln Gln Arg Gln Ile Leu Leu Gly Pro Asn Thr Gly Leu
115 120 125

tca gga gga atg cca ggg gct cta ccc tca ctt cct gga aag atc 430
Ser Gly Gly Met Pro Gly Ala Leu Pro Ser Leu Pro Gly Lys Ile
130 135 140

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cccggtgggg agaattatcc ccacattgtc tcatggaaag actcaacttg caactgtgcc 610
ctccacacta tccttacttc tgtctccact ctgataccag agtgcagcca tgcagacggt 670
tattccagct ctggtcaccc gactcctttc accaaattgc tcctaactgg aagatctcac 730
tttccccttg tgggtagga accgatgcc^a gtgggaggga tgtgcccctg accattaacg 790
actgtttttt ttttttttt ttaaagaatg gagttgttgg ggcgggacat gcacacaatg 850
tgaaacagac aaaatgcatt acacctgttag tgtaaagtgg ccactatgaa tccctatgta 910
tgagaggagg gaggcaggct gcagcttcag ccacagaatg gggactatgg aagacagcag 970
gagctcattt cctctgcaca ttccggctgt tagacctgtg tgtgtgtta aaaaaagaga 1030
agtca^gtgct cacttttgt atttaaatat taaaaatgat tccaactg 1078

<210> 20
<211> 142
<212> PRT
<213> Homo sapiens

<400> 20
Met Ala Ala Ala Val Ala Ala Gly Ala Gly Glu Pro Gln Ser Pro
1 5 10 15

Asp Glu Leu Leu Pro Lys Gly Asp Ala Glu Lys Pro Glu Glu Leu

20

25

30

Glu Glu Asp Asp Asp Glu Glu Leu Asp Glu Thr Leu Ser Glu Arg Leu
35 40 45

Trp Gly Leu Thr Glu Met Phe Pro Glu Arg Val Arg Ser Ala Ala Gly
50 55 60

Ala Thr Phe Asp Leu Ser Leu Phe Val Ala Gln Lys Met Tyr Arg Phe
65 70 75 80

Ser Arg Ala Ala Leu Trp Ile Gly Thr Thr Ser Phe Met Ile Leu Val
85 90 95

Leu Pro Val Val Phe Glu Thr Glu Lys Leu Gln Met Glu Gln Gln Gln
100 105 110

Gln Leu Gln Gln Arg Gln Ile Leu Leu Gly Pro Asn Thr Gly Leu Ser
115 120 125

Gly Gly Met Pro Gly Ala Leu Pro Ser Leu Pro Gly Lys Ile
130 135 140

<210> 21

<211> 1310

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (82)..(1119)

<400> 21

actcatcctg ggctcaggt a agagggcccg agctcgagg cggcacatcc agggggacg 60

ccaagggagc aggacggagc c atg gac ccc gcc agg aaa gca ggt gcc cag 111
Met Asp Pro Ala Arg Lys Ala Gly Ala Gln
1 5 10

gcc atg atc tgg act gca ggc tgg ctg ctg ctg ctg ctt cgc gga 159
Ala Met Ile Trp Thr Ala Gly Trp Leu Leu Leu Leu Leu Arg Gly
15 20 25

gga gcg cag gcc ctg gag tgc tac agc tgc gtg cag aaa gca gat gac 207
Gly Ala Gln Ala Leu Glu Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp
30 35 40

gga tgc tcc ccg aac aag atg aag aca gtg aag tgc gcg ccg ggc gtg 255
Gly Cys Ser Pro Asn Lys Met Lys Thr Val Lys Cys Ala Pro Gly Val
45 50 55

gac gtc tgc acc gag gcc gtg ggg gcg gtg gag acc atc cac gga caa 303
Asp Val Cys Thr Glu Ala Val Gly Ala Val Glu Thr Ile His Gly Gln
60 65 70

ttc tcg ctg gca gtg cgg ggt tgc ggt tcg gga ctc ccc ggc aag aat 351

Phe	Ser	Leu	Ala	Val	Arg	Gly	Cys	Gly	Ser	Gly	Leu	Pro	Gly	Lys	Asn	
75			80			85			90							
gac	cgc	ggc	ctg	gat	ctt	cac	ggg	ctt	ctg	gcg	ttc	atc	cag	ctg	cag	399
Asp	Arg	Gly	Leu	Asp	Leu	His	Gly	Leu	Leu	Ala	Phe	Ile	Gln	Leu	Gln	
95									100					105		
caa	tgc	gct	cag	gat	cgc	tgc	aac	gcc	aag	ctc	aac	ctc	acc	tcg	cgg	447
Gln	Cys	Ala	Gln	Asp	Arg	Cys	Asn	Ala	Lys	Leu	Asn	Leu	Thr	Ser	Arg	
110									115					120		
gcg	ctc	gac	ccg	gca	ggt	aat	gag	agt	gca	tac	ccg	ccc	aac	gac	gtg	495
Ala	Leu	Asp	Pro	Ala	Gly	Asn	Glu	Ser	Ala	Tyr	Pro	Pro	Asn	Gly	Val	
125									130					135		
gag	tgc	tac	agc	tgt	gtg	ggc	ctg	agc	cg	gag	g	tcg	cag	g	gt	543
Glu	Cys	Tyr	Ser	Cys	Val	Gly	Leu	Ser	Arg	Glu	Ala	Cys	Gln	Gly	Thr	
140									145					150		
tcg	ccg	ccg	gtc	gtg	agc	tgc	tac	aac	gcc	agc	gat	cat	gtc	tac	aag	591
Ser	Pro	Pro	Val	Val	Ser	Cys	Tyr	Asn	Ala	Ser	Asp	His	Val	Tyr	Lys	
155									160					165		170
ggc	tgc	tcc	gac	ggc	aac	gtc	acc	ttg	acg	gca	gct	aat	gtg	act	gtg	639
Gly	Cys	Phe	Asp	Gly	Asn	Val	Thr	Leu	Thr	Ala	Ala	Asn	Val	Thr	Val	
175									180					185		
tcc	ttg	cct	gtc	cg	ggc	tgt	gtc	cag	gat	gaa	ttc	tgc	act	cg	gat	687
Ser	Leu	Pro	Val	Arg	Gly	Cys	Val	Gln	Asp	Glu	Phe	Cys	Thr	Arg	Asp	
190									195					200		
gga	gta	aca	ggc	cca	ggg	ttc	acg	ctc	agt	ggc	tcc	tgt	tgc	cag	ggg	735
Gly	Val	Thr	Gly	Pro	Gly	Phe	Thr	Leu	Ser	Gly	Ser	Cys	Cys	Gln	Gly	
205									210					215		
tcc	cgc	tgt	aa	tct	gac	ctc	cgc	aa	aag	acc	ta	ttc	tcc	cct	cga	783
Ser	Arg	Cys	Asn	Ser	Asp	Leu	Arg	Asn	Lys	Thr	Tyr	Phe	Ser	Pro	Arg	
220									225					230		
atc	cca	ccc	ctt	gtc	cg	ctg	ccc	cct	cca	gag	ccc	acg	act	gtg	gcc	831
Ile	Pro	Pro	Leu	Val	Arg	Leu	Pro	Pro	Pro	Glu	Pro	Thr	Thr	Val	Ala	
235									240					245		250
tca	acc	aca	tct	gtc	acc	act	tct	acc	tcg	gcc	cca	gtg	aga	ccc	aca	879
Ser	Thr	Thr	Ser	Val	Thr	Thr	Ser	Thr	Ser	Ala	Pro	Val	Arg	Pro	Thr	
255									260					265		
tcc	acc	acc	aaa	ccc	atg	cca	g	cc	acc	agt	cag	act	ccg	aga	cag	927
Ser	Thr	Thr	Lys	Pro	Met	Pro	Ala	Pro	Thr	Ser	Gln	Thr	Pro	Arg	Gln	
270									275					280		
gga	gta	gaa	cac	gag	gcc	tcc	cg	gat	gag	gag	ccc	agg	ttg	act	gga	975
Gly	Val	Glu	His	Glu	Ala	Ser	Arg	Asp	Glu	Glu	Pro	Arg	Leu	Thr	Gly	
285									290					295		
ggc	gcc	gct	ggc	cac	cag	gac	cgc	agc	aat	tca	ggg	cag	tat	cct	gca	1023
Gly	Ala	Ala	Gly	His	Gln	Asp	Arg	Ser	Asn	Ser	Gly	Gln	Tyr	Pro	Ala	

300

305

310

aaa ggg ggg ccc cag cag ccc cat aat aaa ggc tgt gtg gct ccc aca 1071
Lys Gly Gly Pro Gln Gln Pro His Asn Lys Gly Cys Val Ala Pro Thr
315 320 325 330

gct gga ttg gca gcc ctt ctg ttg gcc gtg gct gct ggt gtc cta ctg 1119
Ala Gly Leu Ala Ala Leu Leu Ala Val Ala Gly Val Leu Leu
335 340 345

tgagcttctc cacctggaaa tttccctctc acctacttct ctggccctgg gtacccctct 1179

tctcatcaact tcctgttccc accactggac tgggctggcc cagcccctgt ttttccaaca 1239

ttccccagta tccccagctt ctgctgcgct ggttgcggc tttggaaat aaaataccgt 1299

tgtatatatt c 1310

<210> 22

<211> 346

<212> PRT

<213> Homo sapiens

<400> 22

Met Asp Pro Ala Arg Lys Ala Gly Ala Gln Ala Met Ile Trp Thr Ala
1 5 10 15

Gly Trp Leu Leu Leu Leu Leu Arg Gly Gly Ala Gln Ala Leu Glu
20 25 30

Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp Gly Cys Ser Pro Asn Lys
35 40 45

Met Lys Thr Val Lys Cys Ala Pro Gly Val Asp Val Cys Thr Glu Ala
50 55 60

Val Gly Ala Val Glu Thr Ile His Gly Gln Phe Ser Leu Ala Val Arg
65 70 75 80

Gly Cys Gly Ser Gly Leu Pro Gly Lys Asn Asp Arg Gly Leu Asp Leu
85 90 95

His Gly Leu Leu Ala Phe Ile Gln Leu Gln Gln Cys Ala Gln Asp Arg
100 105 110

Cys Asn Ala Lys Leu Asn Leu Thr Ser Arg Ala Leu Asp Pro Ala Gly
115 120 125

Asn Glu Ser Ala Tyr Pro Pro Asn Gly Val Glu Cys Tyr Ser Cys Val
130 135 140

Gly Leu Ser Arg Glu Ala Cys Gln Gly Thr Ser Pro Pro Val Val Ser
145 150 155 160

Cys Tyr Asn Ala Ser Asp His Val Tyr Lys Gly Cys Phe Asp Gly Asn
165 170 175

Val Thr Leu Thr Ala Ala Asn Val Thr Val Ser Leu Pro Val Arg Gly
180 185 190

Cys Val Gln Asp Glu Phe Cys Thr Arg Asp Gly Val Thr Gly Pro Gly
195 200 205

Phe Thr Leu Ser Gly Ser Cys Cys Gln Gly Ser Arg Cys Asn Ser Asp
210 215 220

Leu Arg Asn Lys Thr Tyr Phe Ser Pro Arg Ile Pro Pro Leu Val Arg
225 230 235 240

Leu Pro Pro Pro Glu Pro Thr Thr Val Ala Ser Thr Thr Ser Val Thr
245 250 255

Thr Ser Thr Ser Ala Pro Val Arg Pro Thr Ser Thr Thr Lys Pro Met
260 265 270

Pro Ala Pro Thr Ser Gln Thr Pro Arg Gln Gly Val Glu His Glu Ala
275 280 285

Ser Arg Asp Glu Glu Pro Arg Leu Thr Gly Gly Ala Ala Gly His Gln
290 295 300

Asp Arg Ser Asn Ser Gly Gln Tyr Pro Ala Lys Gly Gly Pro Gln Gln
305 310 315 320

Pro His Asn Lys Gly Cys Val Ala Pro Thr Ala Gly Leu Ala Ala Leu
325 330 335

Leu Leu Ala Val Ala Ala Gly Val Leu Leu
340 345

<210> 23
<211> 781
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (342)..(539)

<400> 23
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aaagcggcgg cgacggcggc gcgagaacga cccggcggcc agttctcttc ctcctgcgca 120
cctgcctgc tcggtcagtc agtcggcggc cggcgcccgg cttgtgctca gacctcgcc 180
ttgcggcgcc caggcccagc ggccgtagct agcgtctggc ctgagaacct cggcgctccg 240
gcggcgcggg caccacgagc ggagcctcgc agcggctcca gaggaggcag gcgagtgagc 300
gagtccgagg ggtggccggg gcaggtggtg gcccggcaa g atg gtc gcc aag caa 356
Met Val Ala Lys Gln

1 5

agg atc cgt atg gcc aac gag aag cac aac agc aag aac atc acc cag cgc 404
Arg Ile Arg Met Ala Asn Glu Lys His Ser Lys Asn Ile Thr Gln Arg
10 15 20

ggc aac gtc gcc aag acc tcg aga aat gcc ccc gaa gag aag gcg tct 452
Gly Asn Val Ala Lys Thr Ser Arg Asn Ala Pro Glu Glu Lys Ala Ser
25 30 35

gta gga ccc tgg tta ttg gct ctc ttc att ttt gtt gtc tgt ggt tct 500
Val Gly Pro Trp Leu Leu Ala Leu Phe Ile Phe Val Val Cys Gly Ser
40 45 50

gca att ttc cag att att caa agt atc agg atg ggc atg tgaagtgact 549
Ala Ile Phe Gln Ile Ile Gln Ser Ile Arg Met Gly Met
55 60 65

gaccttaaga tgtttccatt ctcctgtgaa ttttaacttg aactcattcc tcatgtttga 609
taccctgggtt gaaaacaatt cagtaaagca tcctgcctca gaatgacttt cctatcatgc 669
ttcatgtgtc attccaaggt ttcttcatga gtcattccaa gtttctagt ccataccaca 729
gtgccttgca aaaaacacca catgaataaa gcaataaaat ttgattgtta ag 781

<210> 24

<211> 66

<212> PRT

<213> Homo sapiens

<400> 24

Met Val Ala Lys Gln Arg Ile Arg Met Ala Asn Glu Lys His Ser Lys
1 5 10 15

Asn Ile Thr Gln Arg Gly Asn Val Ala Lys Thr Ser Arg Asn Ala Pro
20 25 30

Glu Glu Lys Ala Ser Val Gly Pro Trp Leu Leu Ala Leu Phe Ile Phe
35 40 45

Val Val Cys Gly Ser Ala Ile Phe Gln Ile Ile Gln Ser Ile Arg Met
50 55 60

Gly Met

65

<210> 25

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chimeric
DNA-RNA oligonucleotide

<400> 25
gggaaattcg agga

14

<210> 26
<211> 162
<212> PRT
<213> Homo sapiens

<400> 26
Met Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
1 5 10 15

Phe Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr
20 25 30

Val Val His Leu Ala Pro Pro Ser Glu Val Ala Gly Ala Gly Ala Ala
35 40 45

Ser Val Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu
50 55 60

Leu Tyr Asp Val Ala Gly Ser Asp Lys Tyr Gln Val Asn Asn Lys His
65 70 75 80

Asp Asp Lys Tyr Ser Pro Leu Pro Cys Thr Lys Ile Ile Gln Arg Ala
85 90 95

Glu Glu Leu Val Gly Gln Glu Val Leu Tyr Lys Leu Thr Ser Glu Asn
100 105 110

Cys Glu His Phe Val Asn Glu Leu Arg Tyr Gly Val Ala Arg Ser Asp
115 120 125

Gln Val Arg Asp Val Ile Ile Ala Ala Ser Val Ala Gly Met Gly Leu
130 135 140

Ala Ala Met Ser Leu Ile Gly Val Met Phe Ser Arg Asn Lys Arg Gln
145 150 155 160

Lys Gln

<210> 27
<211> 162
<212> PRT
<213> Homo sapiens

<400> 27
Met Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
1 5 10 15

Phe Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr
20 25 30

Val Val His Leu Ala Pro Pro Ser Glu Val Ala Gly Ala Gly Ala Ala
35 40 45

Ser Val Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu
50 55 60

Leu Tyr Asp Val Ala Gly Ser Asp Lys Tyr Gln Val Asn Asn Lys His
65 70 75 80

Asp Asp Lys Tyr Ser Pro Leu Pro Cys Thr Lys Ile Ile Gln Arg Ala
85 90 95

Glu Glu Leu Val Gly Gln Glu Val Leu Tyr Lys Leu Thr Ser Glu Asn
100 105 110

Cys Glu His Phe Val Asn Glu Leu Arg Tyr Gly Val Ala Arg Ser Asp
115 120 125

Gln Val Arg Asp Val Ile Ile Ala Ala Ser Val Ala Gly Met Gly Leu
130 135 140

Ala Ala Met Ser Leu Ile Gly Val Met Phe Ser Arg Asn Lys Arg Gln
145 150 155 160

Lys Gln

<210> 28

<211> 64

<212> PRT

<213> Nematode

<400> 28

Met Ala Pro Lys Gln Arg Met Thr Leu Ala Asn Lys Gln Phe Ser Lys
1 5 10 15

Asn Val Asn Asn Arg Gly Asn Val Ala Lys Ser Leu Lys Pro Ala Glu
20 25 30

Asp Lys Tyr Pro Ala Ala Pro Trp Leu Ile Gly Leu Phe Val Phe Val
35 40 45

Val Cys Gly Ser Ala Val Phe Glu Ile Ile Arg Tyr Val Lys Met Gly
50 55 60